

In the Claims

Rewrite claims 2, 13, 20-27 and 30 as follows:

2. (thrice amended) A process for the preparation of a transgenic plant, which process comprises:

- (i) transforming a plant cell with a chimaeric gene comprising (a) a promoter operably linked to (b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes for an enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, [adenine] adenosine diphosphoglucose pyrophosphorylase, sucrose synthase, [6-phospho-fructokinase] 6- phosphofructokinase (pyrophosphate) and sucrose phosphate synthetase; whereby there is caused a modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar, and
- (ii) regenerating a plant from the transformed cell.

*E 2*

13. (thrice amended) A transgenic plant which harbors in its cells a chimaeric gene which comprises;

(a) a promoter operably linked to

(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes an enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, 6-phosphofructokinase (pyrophosphate), [adenine] adenosine diphosphoglucose [diphosphoglucose] pyrophosphorylase, sucrose synthase and sucrose phosphate synthetase; and which is capable of being expressed in the cells of the plant thus to cause a modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.

*E 3*

20. (twice amended) A transgenic potato plant which harbors in its cells a chimaeric gene, which comprises;

(a) a promoter operably linked to

(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes [adenine] adenosine diphosphoglucose pyrophosphorylase [pyrophosphorylase]; said gene being capable of expression in the cells of the transgenic potato plant.

10/15/96 . DCF  
10/15/96 (74)  

---

21. (twice amended) A transgenic potato plant according to claim 20 wherein the [fragment] gene also comprises a coding sequence which encodes for a second enzyme.

22. (twice amended) A process according to claim 2, wherein the [fragment] gene encodes for [2] two or more of the enzymes selected.

23. (twice amended) A chimaeric gene [as defined in] according to claim [17] 2, wherein the [fragment] gene encodes for [2] two or more of the enzymes selected.

24. (twice amended) A transgenic plant according to claim 13 wherein the [fragment] gene encodes for [2] two or more of the enzymes selected.

25. (twice amended) A transgenic plant which harbors in its cells a chimaeric gene, which comprises;

(a) a promoter operably linked to

(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes for phosphofructokinase and the gene comprising a coding sequence encoding for a second enzyme selected from the group consisting of pyruvate kinase, acid invertase, starch synthase, [adenine diphosphogluucose] adenosine diphosphoglucose pyrophosphorylase,

*E<sup>4</sup>*  
sucrose synthase, 6-phosphofructokinase (pyrophosphate) and sucrose phosphate synthetase;

said gene being capable of being expressed in the cells of the transgenic plant.

26. (twice amended) A transgenic potato plant which harbors in its cells a chimaeric gene, which comprises:

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes [adenine diphosphoglucone] adenosine diphosphoglucose pyrophosphorylase and the gene comprising a coding sequence encoding for a second enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, sucrose synthase, 6-phosphofructokinase (pyrophosphate) and sucrose phosphate synthetase; said gene being capable of being expressed in the cells of the transgenic potato plant.

27. (amended) A transgenic potato plant which harbors in its cells a chimaeric gene, which comprises:

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes for acid invertase, and the gene comprising a coding sequence encoding for a second enzyme, said gene being capable of expression in the cells of the transgenic potato plant.

30. (amended) A transgenic plant which harbors in its cells a chimaeric gene comprising;

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment which comprises a coding sequence for an enzyme in the pre-existing plant pathway of glycolysis or the synthesis or degradation of starch, sucrose or reducing sugar, and [the product] of which causes modification of the amount of metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.

Enter new claims 31-59, inclusive, as follows:

E 6  
31. The process of claim 2 wherein the enzyme selected is phosphofructokinase.

2  
32. The process of claim 2 wherein the enzyme selected is pyruvate kinase.

33. The process of claim 2 wherein the enzyme selected is starch synthase.

34. The process of claim 2 wherein the enzyme selected is adenosine diphosphoglucose pyrophosphorylase.

35. The process of claim 2 wherein the enzyme selected is sucrose synthase.

36. The process of claim 2 wherein the enzyme selected is acid invertase.

37. The process of claim 2 wherein the enzyme selected is 6-phosphofructokinase (pyrophosphate). *2*

38. The process of claim 2 wherein the enzyme selected is sucrose phosphate synthetase. *E6*

39. The plant of claim 13 wherein the enzyme selected is phosphofructokinase. *31*

40. The plant of claim 13 wherein the enzyme selected is pyruvate kinase.

41. The plant of claim 13 wherein the enzyme selected is starch synthase. *2*

42. The plant of claim 13 wherein the enzyme selected is acid invertase.

43. The plant of claim 13 wherein the enzyme selected is adenosine diphosphoglucose pyrophosphorylase. *31*

44. The plant of claim 13 wherein the enzyme selected is sucrose synthase.

45. The plant of claim 13 wherein the enzyme selected is 6-phosphofructokinase (pyrophosphate).

46. The plant of claim 13 wherein the enzyme selected is sucrose phosphate synthetase.

E6  
47. A process according to claim 2, wherein said gene comprises a coding sequence encoding for a second enzyme.

2  
48. A process according to claim 2, wherein said fragment is expressed in a tuber of said regenerated plant.

49. A process according to claim 2, wherein said fragment is expressed in a seed of said regenerated plant.

50. A transgenic tuber which harbors in its cells a chimaeric gene which comprises;

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes an enzyme

*E6*

selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, 6-phosphofructokinase (pyrophosphate), adenosine diphosphoglucose pyrophosphorylase, sucrose synthase and sucrose phosphate synthetase; and which is capable of being expressed in the cells of the tuber.

51. A transgenic seed which harbors in its cells a chimaeric gene which comprises;

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes an enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, 6-phosphofructokinase (pyrophosphate), adenosine diphosphoglucose pyrophosphorylase, sucrose synthase and sucrose phosphate synthetase; and which is capable of being expressed in the cells of the seed.

52. A transgenic plant according to claim 13, wherein the gene encodes for a second enzyme.

*E6*

53. A transgenic tuber which harbors in its cells a chimaeric gene comprising;

- (a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment which comprises a coding sequence for an enzyme in the pathway of glycolysis or the synthesis or degradation of starch, sucrose or reducing sugar and which causes modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.
- 7*

54. A transgenic seed which harbors in its cells a chimaeric gene comprising;

- (a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment which comprises a coding sequence for an enzyme in the pathway of glycolysis or the synthesis or degradation of starch, sucrose or reducing sugar and which causes modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.

55. A transgenic plant according to claim 30, wherein said gene encodes for a second enzyme.